FIG.1a.

Synthetic DNA Substrates Mimicking Transcriptional
Cis- Regulatory Elements

GC-box a:	5' -GGGAATTCAAGGGGCGGGGCAAGGATCCAG -3'
GC-box b:	5' -CTGGATCCTTGCCCCGCCCCTTGAATTCCC -3'
GC-box b MET:	5' -CTGGATCCTTGCCC^{m}CGCCCCTTGAATTCCC -3'
CRE a:	5' -GGGAATTCAAATGACGTCAAAAGGATCCAG -3'
CRE b:	5' -CTGGATCCTTTTGACGTCATTTGAATTCCC -3'
CRE a MET:	5' -GGGAATTCAAATGA^{m}CGTCAAAAGGATCCAG -3'

FIG. 1b.

NAME	NUCLEO-TIDES	Sequence	Kii (nM)	IC50 (nM)
GC-Box b (SEQ ID NO: 10)	30	5'-CTGGATCCTTGCCCCGCCCCTTGAATTCCC-3	6800	
GC-Box bMET (SEQ ID NO: 10)	30	5'-CTGGATCCTTGCCCmCGCCCCTTGAATTCCC-3'	20	15
GC Box $_p$MET (SEQ ID NO: 10)	30	5'-CTGGATCCTTGCCCmCGCCCCTTGAATTCCC-3'		5
GC-Box cMET (SEQ ID NO: 13)	50	5'- CCTACCCACCCTGGATCCTTGCCCmCGCCCCTTGAATTCCCAACCCTCCAC-3'		30
GC Box dMET (SEQ ID NO: 14)	22	5'-ATCCTTGCCCmCGCCCCTTGAAT-3'		50
GC-Box eMET (SEQ ID NO: 15)	14	5'TTGCCCmCGCCCCTT-3'		150
CRE aMET (SEQ ID NO: 11)	30	5'-GGGAATTCAAATGAmCGTCAAAAGGATCCAG-3'		> 300

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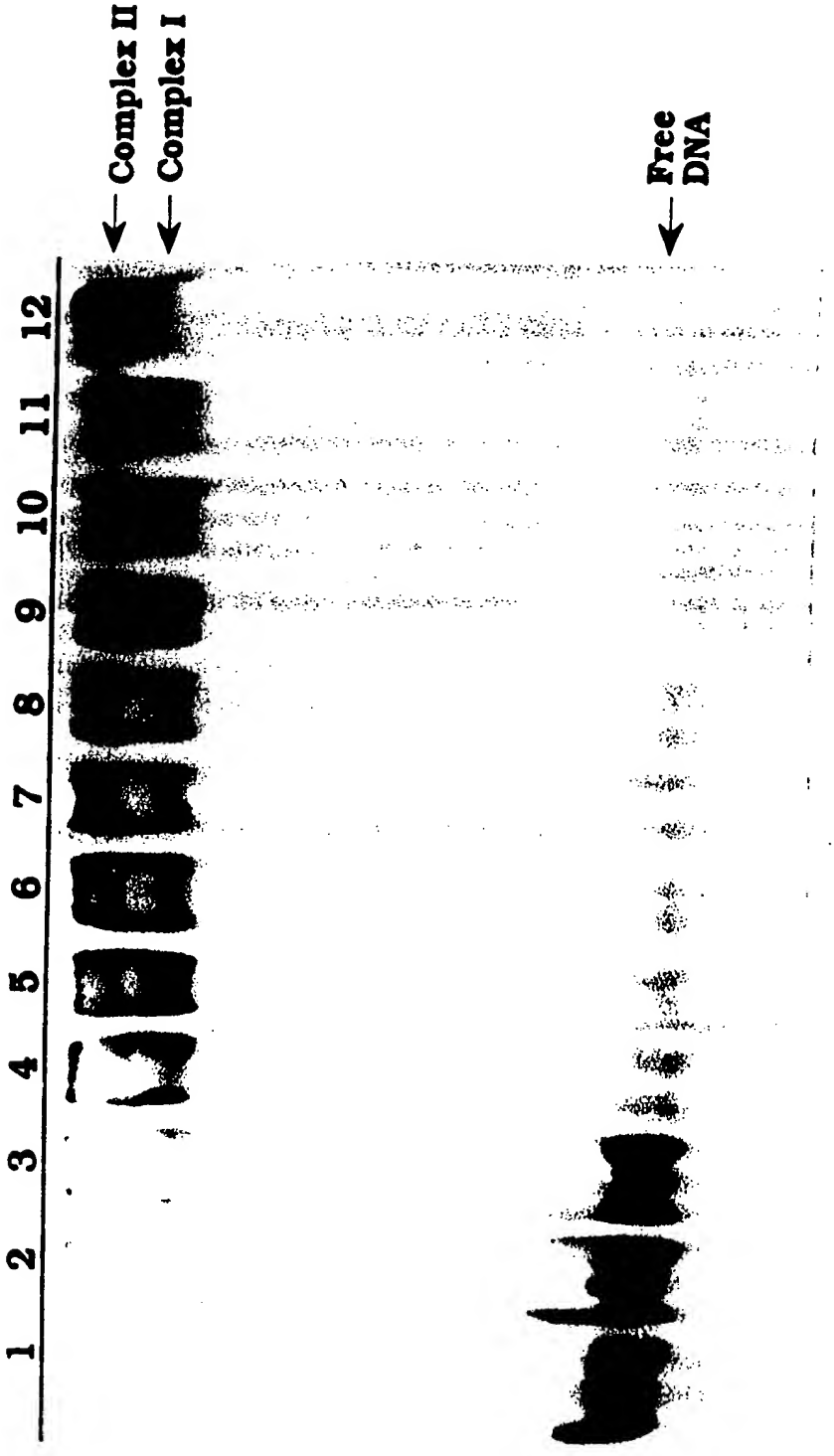

FIG. 2.

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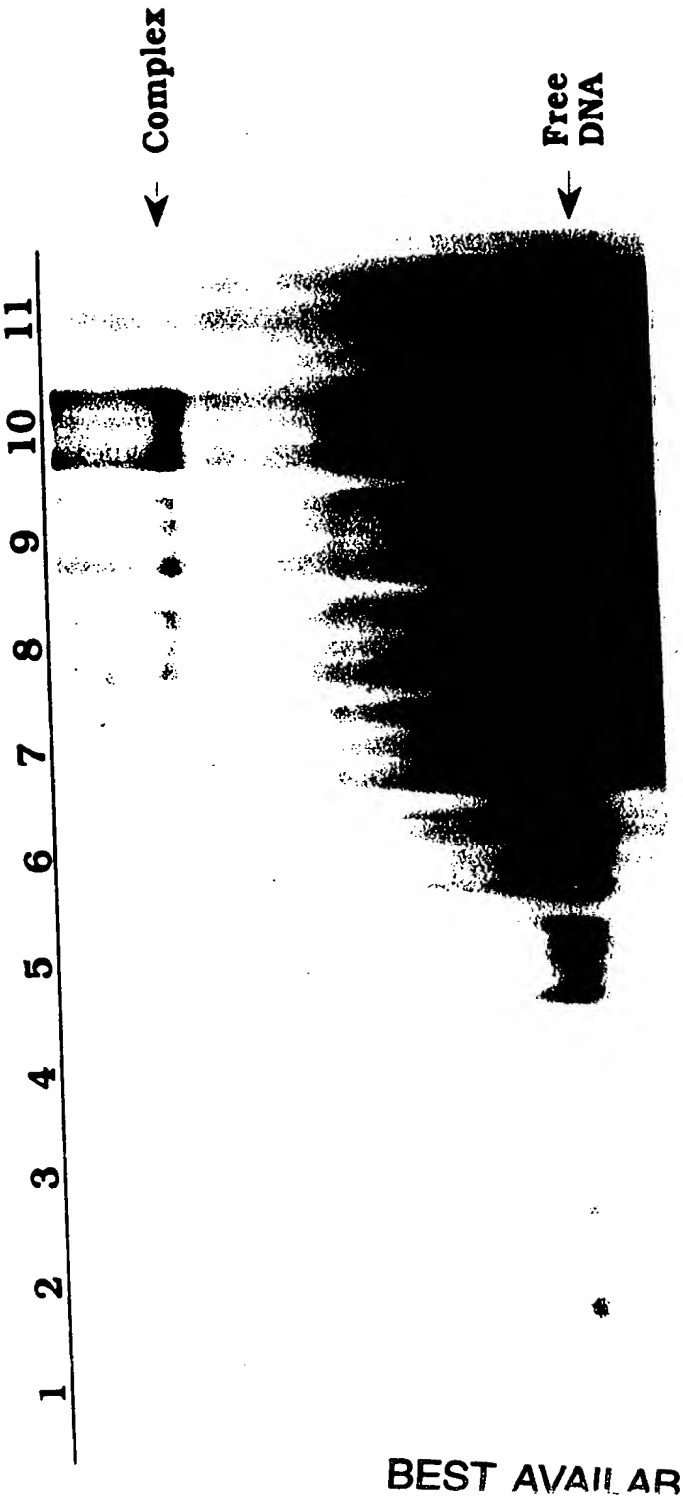

FIG. 3.

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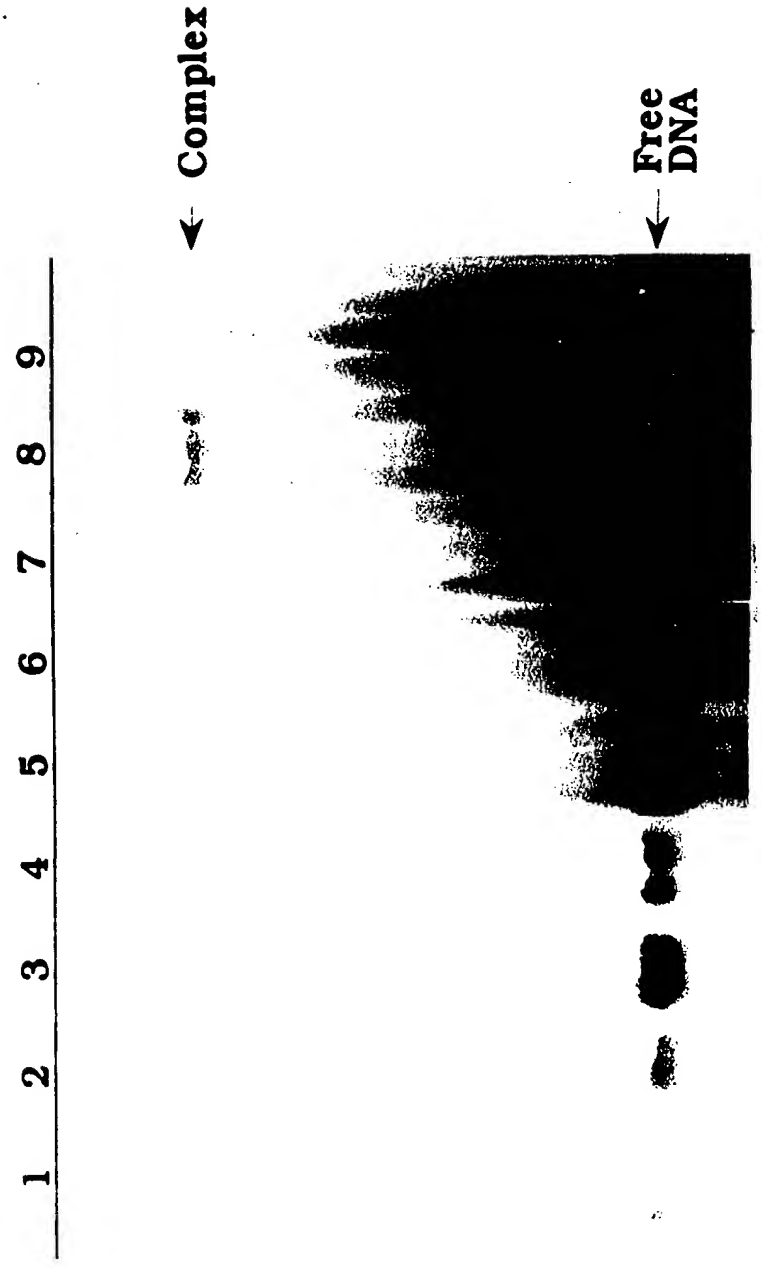

FIG. 4

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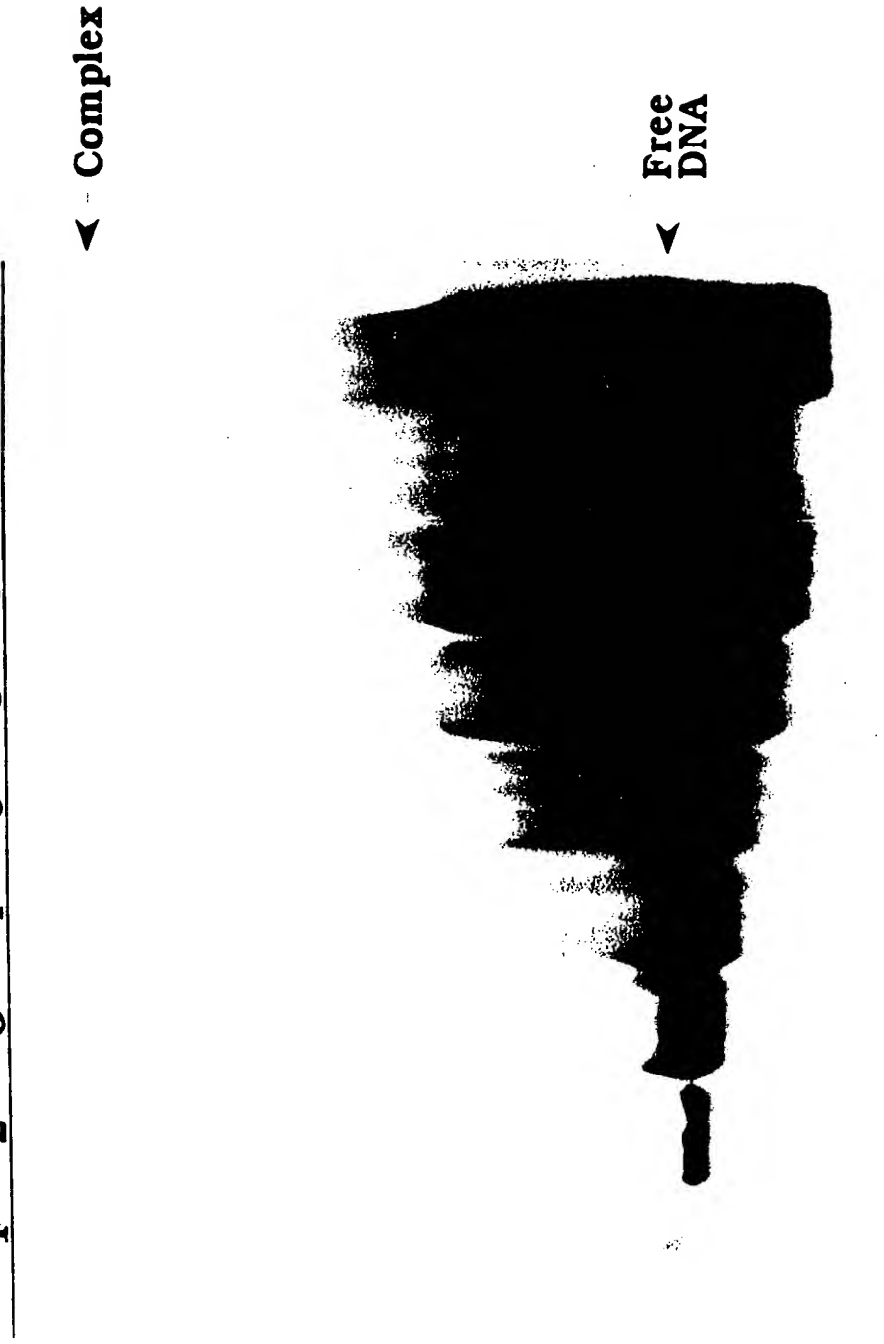

FIG 5

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FIG. 6.

Primer C

5'-GGGAATTCATGGATCCTAAANNNNNNNNNNNNCGNNNNNNNNNNTTTCAAGCTTGTGAATTCCC-3'

3'-CCCTTAAGTACCTAGGATTTNNNNNNNNNNNNGCNNNNNNNNNNAAAGTTCGAACACTTAAGGG-5'

Primer D

FIG.7a.

STARTING POPULATION

GTGGGATGGGAACGAGTTGAGGAGGG
AGTGGTATGTATCGATTATACGTTGGG
GGAGGAAGTTTACGTATGGTATGGGG
TGGGAGGGGATTCGAGGTGAGAGTTG
ATAAAGTATTAGCGTAAGAGATGAAG
TGGAGGAGTTTACGGTGTAATTGTTT
GGAGTAGGTAGACGTTAAGTATGATG
GTGGGAAGGGGACGAATTTGAAGGTG
TGGTAATGTATTCGTAAATGTAAGGG
TAATAGGGGAGACGTAAATGTAAGGG
GAGTGTAGAAGTCGTAATAGATTTAG
TGAGTAGGAAAGCGAAGAGGTGTTGG

FIG.7b.

GENERATION 1

TAGGTATTGGGGCGGAAGGTGGGTGG
GGGGGTATAATACGGTGTTGGTAGGG
GGGTTGGGGTTTCGTGTGGGGGGTGT
TGTGGGTATGGGCGGTGATAGTGAAG
GGATGATGGGGTCGAGAGTGGTGGTG
TAGTGGGTGGAGCGAGTGGTGGTTGG
AGGGTGGGTGGGCGGAGTTGTTGTTG
GTGAGGAGGGAGCGGGAATGGGGGTG
GGGGGTGGGGAGCGGAGGGGGGTGAG
TGTTGGAGGGGGCGAAGGTGGTTTTG

FIG.7c.

GENERATION 3

GGGGGGGGGGGGCGAGGGGTAGATGG
GGGGGAGGGGTTCGGTGATAGGTAGG
GGGGGGGGGGGTACGTGGGATGGTATG
GTGTAGGGAGTGCGAGGGGGTGTAAA
GGGGGGGGGGTAGCGGTTAGATGGTGG
GGGGTGAGGGGGCGGGGGTTAGTGGG
GAGGGGGGGGTTGCGTAGGGGGGTGGG
TGTGGAGGTGGGCGGGAAAGGTGATG
GGGGGGATGGGACGGATGGGGGGGGG
GGGGGTGGGGTGCGAGAGAGTTGGGG
GAGGGGTGGAGGCGGAGGTGGGTTGG
GGGGGGGGGGGGCGATAAGGGTGTG

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FIG.7d.

GENERATION 5

G#	GpT	TpG		TpG	GpT	G#
11		•	TGGGGGGGGGGGCGGGGGAGTTTGA	•	•	7
11			GGGGGGGAGGGGCGGATAGTTGTGTG	•••	•••	5
10	••	••	GGGTGGGGTGGGCGGTGGGGGTGTGGG	•••	•••	9
10			GAGGGGGGGGAGCGGAGGGGGTTGGG	•	•	9
10			GGGGGGGAAGGGCGTGGGGTTGGGTG	•••	••	8
10			-GGGAGGGGGGGCGATGGGGGTGGTGG	•••	••	8
10	••	••	GGGTGGGGGTGGCGTTGTGGGGTGGGG	•••	••	8
10	••	•	GGGAGGGGGTGGCGGTGGGTATGTGG	•••	•••	7
10	•	•	GGGGAGGGTGGGCGGGGTATGGAGTGG	••	••	7
10	•	•	GGGGGGGGAGTGCGTTGATGGGTGTG	•••	••	6
9	•	•	GGGGGGGGTGGATCGTGGGGGGGAGGGG	•		10
9	••	••	GGGGTAGGGTGGCGGGGGGGGGTATGG	•	•	9
9	•	••	GGGATGGGGGGTGCGGGGGTATGGGGGG	•	•	9

FIG. 7e.

GENERATION 5

G#	GpT	TpG		TpG	GpT	G#
9	•		GGGAGGGGGTAGCGGGAGTGTGTGTG	•••	••••	7
9	•		GGGGGTAAGGGGCGTAAGAATGGGGG	•		6
9	••	•	GGGGGGGTGGTTCGGTAATGGGGGGT	•	••	7
9	•	•	GGTGGGAGAGGGCGTGGTGTAGGTAG	••	•••	6
9	••	•	GGGGGGGGTGTACGAGGTTTGTGTGG	•••	•••	6
9	•	••	TGGTGGAGGGGGCGAAGAAGTGTGTG	•••	•••	5
9	•	••	GGGGGTGGGATGCGGAATAAGGATGG	•		6
9		•	TGAGGGGGAGGGCGAATAGATGGTGG	••	•	7
8	•		GGGGGGAGTAAGCGGGGGGTGTGGTGG	•••	•••	9
8	•	••	TGAAGGGGGGGTGCGGGGGTGTGGGGG-	••	••	9
8	••	•••	GTGGTGATGGGGGCGGGGGTGGTAGTGG	••	•••	8
8	•	•	TGGAGGGGGTAGGCGTGGGGGTGATGGG	•••	•	8

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FIG. 7f.

GENERATION 5

G#	GpT	TpG		TpG	GpT	G#
8	••	•	GGTAGGGAGTGGCGGGTGGTGATGGG	•••	••	8
8	••	•	GGGTGTAGAGGGCGGGAGTAGAGGGG		•	8
8	••	••	GGGTGGGTTTGGCGTAATTGTGTGGG	•••	••	7
8	•••	•••	GGGTGTGTTGGGCGTGGGGTATGTAG	••	••	6
7		••	TGGGGAGAATGGCGGGGGGGTGGTGGG	••	••	10
7	•	••	TATGGTGGGAGGCGGGGGGGGGTTGG	•	•	10
7		•	TGGGGAAAGAGGCGTGAGTGGGGGGG	••	•	9
7	•	•	TGTAGGGGAGGACGGGGGGATGGGGTG	••	•	9
7	••	••	GGGTGGGTAATGCGTAGGGTGGGGGG	•	•	9
7	•••	••	GTGTGGGTAAGGCGGTATGGGGGTGG	••	••	8
7	••	•••	TGGAGGGTGTTGCGGTGAGGTGGTGG	•••	•••	8
7	•••	•••	GGTGGTGGTGATCGGGGGTTGTGATGG	•••	••	7

FIG.7g.

GENERATION 5

G#	GpT	TpG		TpG	GpT	G#
7	..	.	GGGGGTAAAGTGCGGGTGGTTGATGG	...	..	7
7	...	...	GTGGAGGTGTTGCGTAGTGTGGGAGG	..	..	7
7	..	..	GTGGGGAATGGTCGGTTATGGTGGGG	..	..	7
7	..	..	GGGATGTGGTAGCGGGGGTGTGTTAG	..	...	7
7	..	..	GGGGTAGGAGTTCGTAGGGGGTGTGTT	..	...	6
7	..	..	GAGGTGGTGGATCGGGATGATGGATT	..		5
6		.	TGGGGGGAAATACGGGGAGGGGTGGTA	.	..	8
6	..		GGAGTAGGGTTACGTGGTGGTAATGG	...	..	6
6	.		GAGGAGTAAAGGCGTGTGTTGTGGTG	....	....	6
6	.	....	TGGATGAGAGTGCGTGTATGATAAGG	..	.	4
5	..	.	AGGGTTAGTGAACGGGGGGGGAGGTGG	.	.	10
5	.		GAGAAGGGTAAACGTGGGGGAGGGGA	.		9

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FIG.8a.

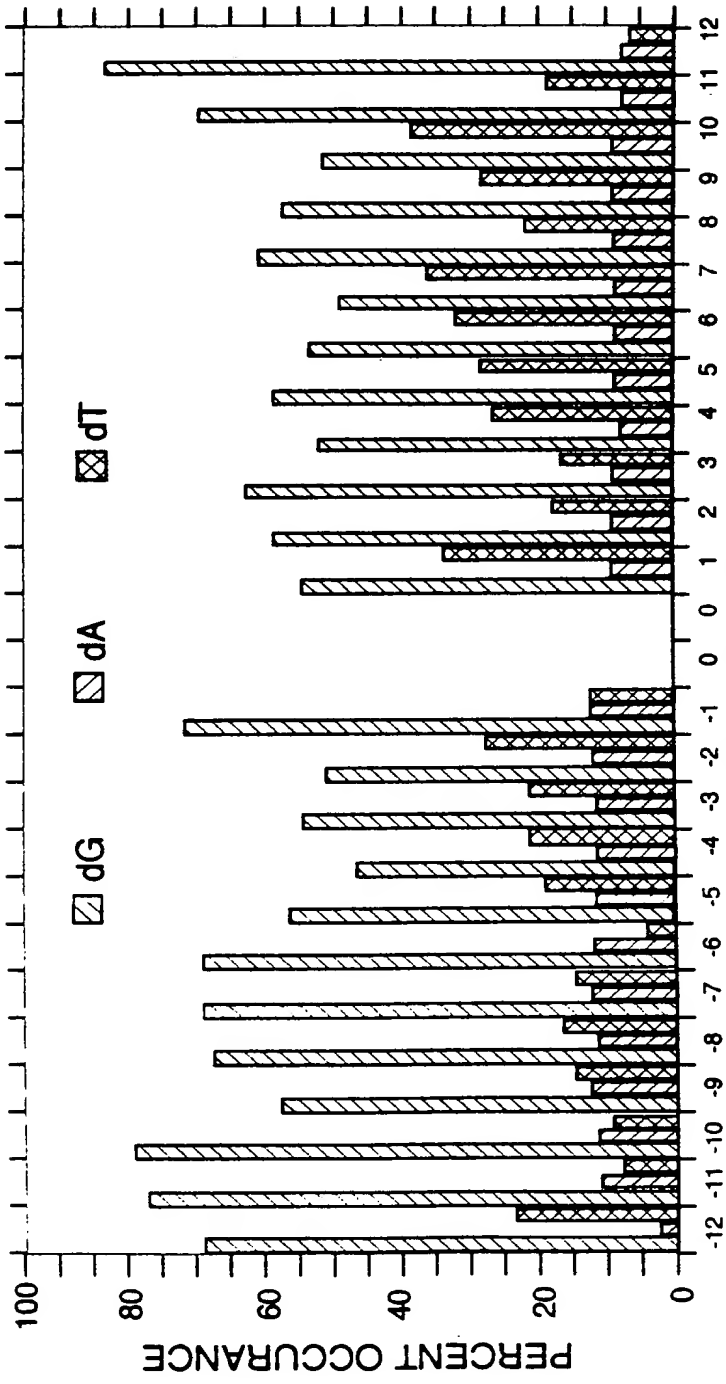

FIG.8b.

	-12	-11	-10	-9	-8	-7	-6	-5	-4	-3	-2	-1	C	G	1	2	3	4	5	6	7	8	9	10	11	12
%G	73	82	84	61	71	73	73	59	49	57	53	76	0	100	57	61	65	53	61	55	51	63	59	53	73	88
%A	2	10	6	22	10	10	22	20	29	20	18	12	0	0	10	20	18	20	10	12	12	14	12	6	6	6
%T	25	8	10	16	18	16	4	20	22	22	29	12	0	0	33	18	16	27	29	33	37	22	29	41	20	6
%C	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0

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FIG.9a

DEFINITION Lyt-2.2 gene, T- cell differentiation antigen, 3' UTR.
ACCESSION GB_RO:MMLYT22

```
          TGGGGGGGGGGCGGGGGAGTTTGA
          |||||||||||||||||||   |||
GAACAATGGGGGCGCTGGGGGGGGGGCGGGGGGCTTTAGCTATGTCAGAATTCA
   5100      5110      5120      5130      5140
```

DEFINITION homeo box 2.6 (Hox-2.6) mRNA
ACCESSION GB_RO:MUSHOX26

```
          GGGATGGGGGTGCGGGGTATGGGGGG
           || |||||||||||||||||||| ||
GGGGAACAGCGAGCACCGAAGGGGGTGCGGGGTATGGGAGGGTCCCCGGGCTTGAGC
 870       880       890       900       910       920
```

DEFINITION growth arrest-specific promoter gene, gas-1
ACCESSION GB_RO:MMGAS1PRA

```
          GGTGGTGGTGATCGGGGTTGTGATGG
          ||||||  | | |||  ||||||| ||
TGTCCTTCTTGTGGTGGTGGTAGAGGTCGTGGTTGTGATGGTGGCTCGGTGTGTGT
   2480      2490      2500      2510      2520
```

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FIG.9b.

DEFINITION pim-1 proto-oncogene, pim-1 protein kinase, CpG island, 5' UTR region.
ACCESSION GB_RO:MUSPIM1

```
                    GAGGGGGGGGAGCGGAGGGGGTTGGG
                    ||||||| ||||||||||||| ||
GAGGGGTGTAGCCGCGAGGGGGCGGAGCGGAGGGGGAGGGCCCTGGTCCCGCCGCC
      1500      1510      1520      1530      1540
```

DEFINITION neuronal dihydropyridine-sensitive L-type calcium channel alpha-1 subunit mRNA, 3' UTR.
ACCESSION GB_RO:MUSDHPCC

```
                    CCCCACCCACAACGCCACCCCCACCC
                    ||||||| | ||||||||||| |||
TCTTTAAATGGTGCGGTCCACCCCCACCGCCACCCCCACCCCCCACTGGAGCAAGG
  8330      8340      8350      8360      8370      8380
```

FIG.9c.

HUMAN SEQUENCES

DEFINITION Huntington's Disease Region, chromsome 4p16.3.
ACCESSION GB_PR:HSL1C2

DEFINITION Human Down Syndrome region of chomosome 21.
ACCESSION GB_HTG:HSAC00002

DEFINITION upstream region of HoxA7 gene, CpG island.
ACCESSION GB_PR:HSHCRDNA

DEFINITION chromosome 22 CpG island DNA
ACCESSION GB_PR:HS303B3

DEFINITION CpG island DNA.
ACCESSION GB_PR:HS167B9F

DEFINITION Y chromosome sex determining region, Yp pseudoautosomal boundary, PAB1.
ACCESSION GB_PR:HSCAMF3X1

DEFINITION creatine transporter and paralogous genes, pericentomeric repeats on chromosome 16.
ACCESSION GB_PR:HSU41302

DEFINITION cathepsin D (cat D) gene, exon 5.
ACCESSION GB_PR:HUMCATD3

FIG.9d.

DEFINITION argininosuccinate synthetase gene 5' end, CpG island
ACCESSION GB_PR:HSASG5E

DEFINITION argininosuccinate synthetase gene 5' end, CpG island
ACCESSION GB_PR:HUMAS1

DEFINITION vimentin gene, 5' regulatory region, CpG island.
ACCESSION GB_PR:HUMVIM

DEFINITION vimentin gene, exon 1, 5' end CpG island.
ACCESSION GB_PR:HUMVIM02

DEFINITION vimentin gene, 5' end, CpG island.
ACCESSION GB_PR:HUMVIMAA

DEFINITION vimentin gene, 5' end, CpG island
ACCESSION GB_PR:HSVIM5RR

DEFINITION chromosome 22 DNA *SEQUENCING IN PROCESS* , CpG island
ACCESSION GB_HTG:HS17OA21

FIG. 10.

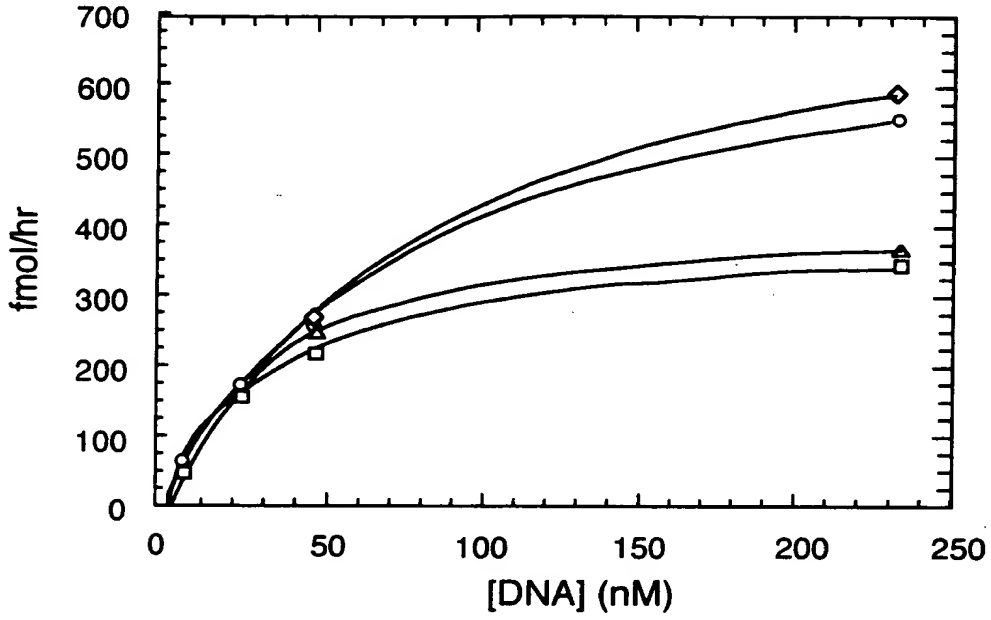

FIG. 13.

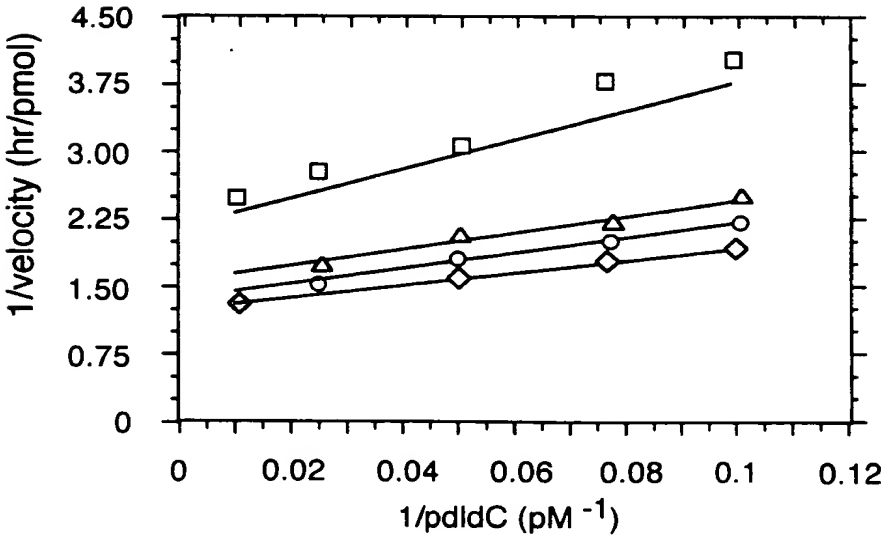

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FIG. 11.

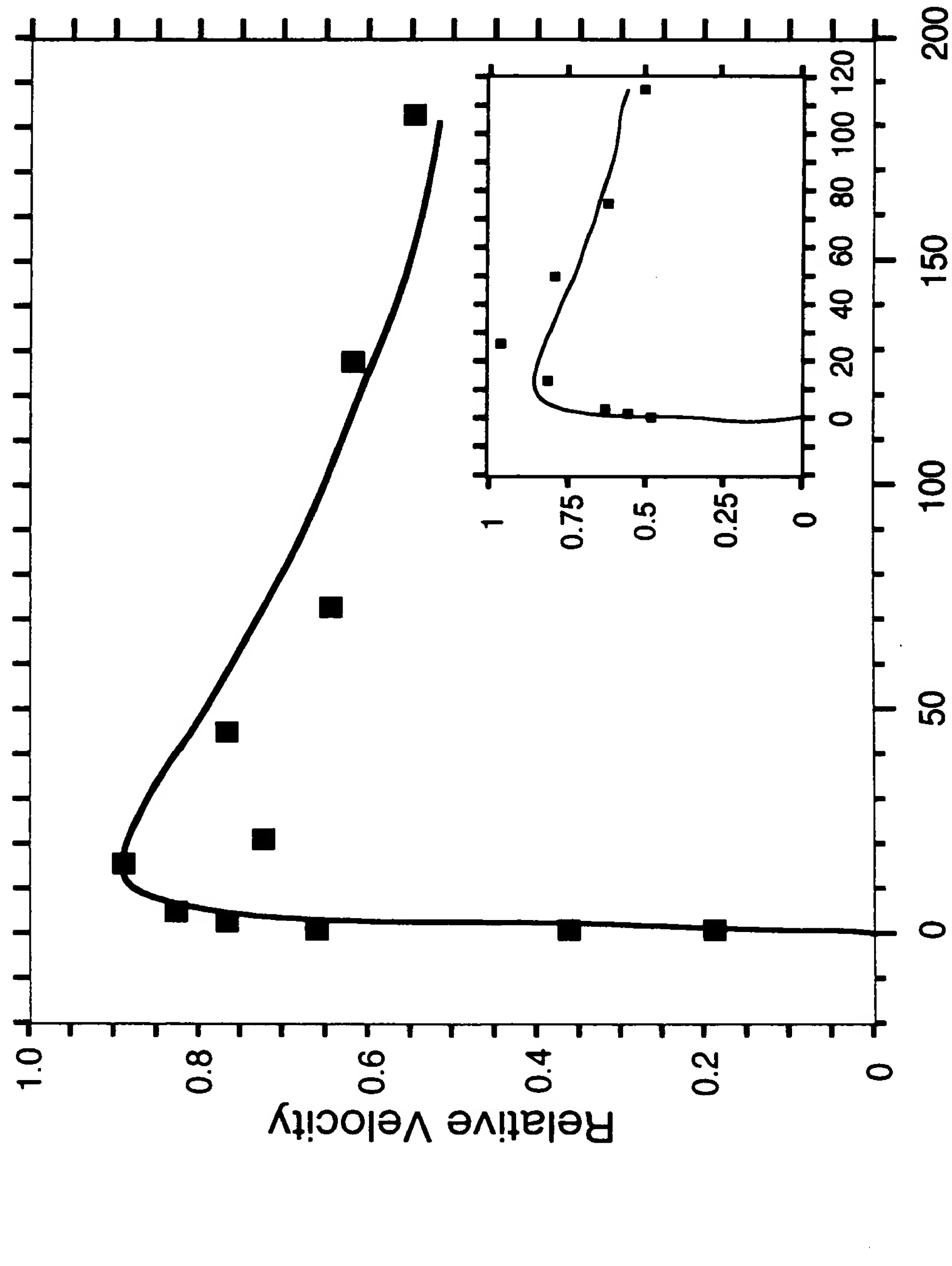

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FIG.12a.

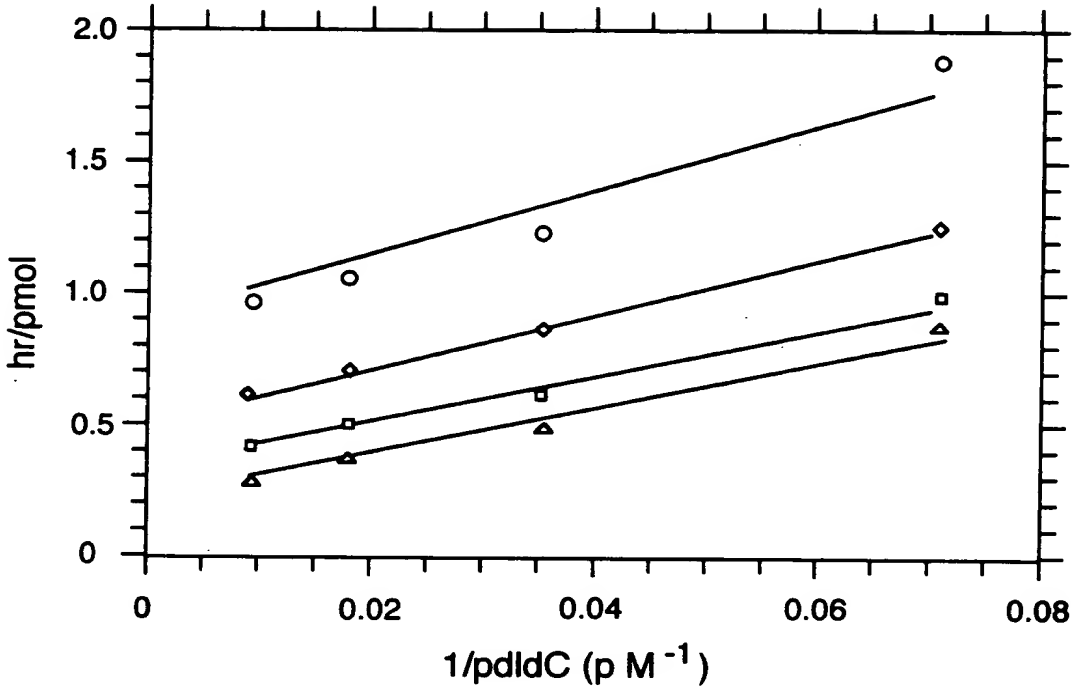

FIG.12b.

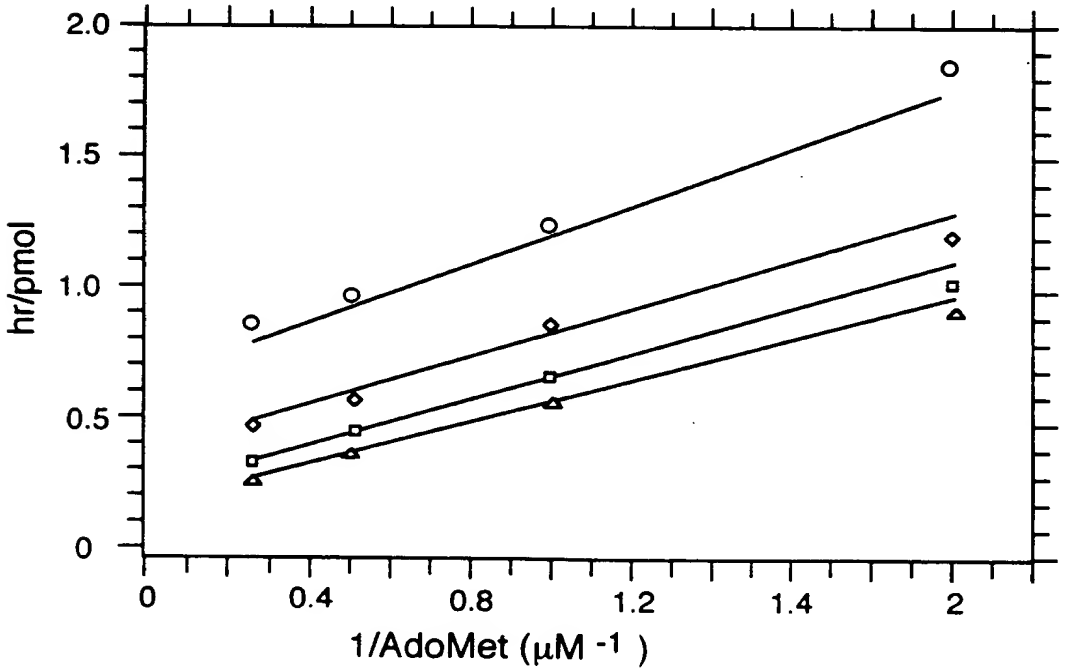

FIG.14.

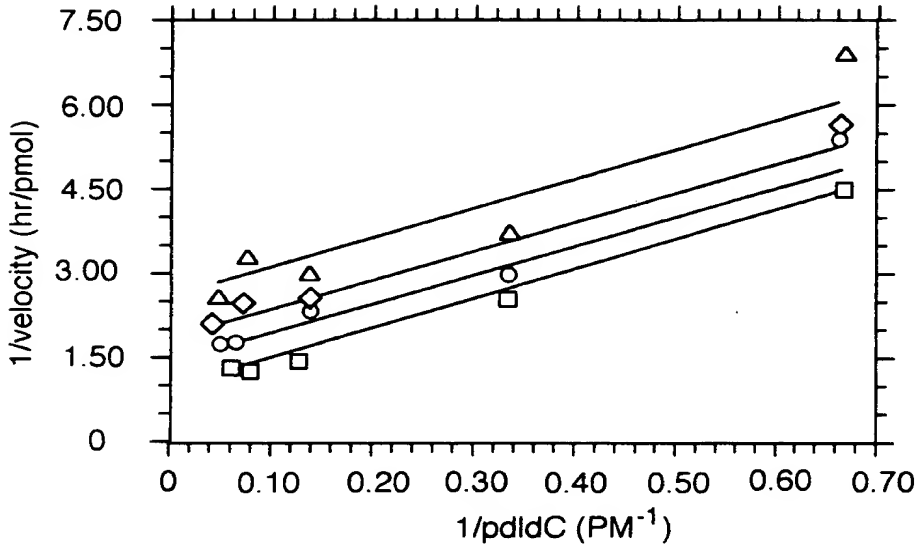

FIG.16.

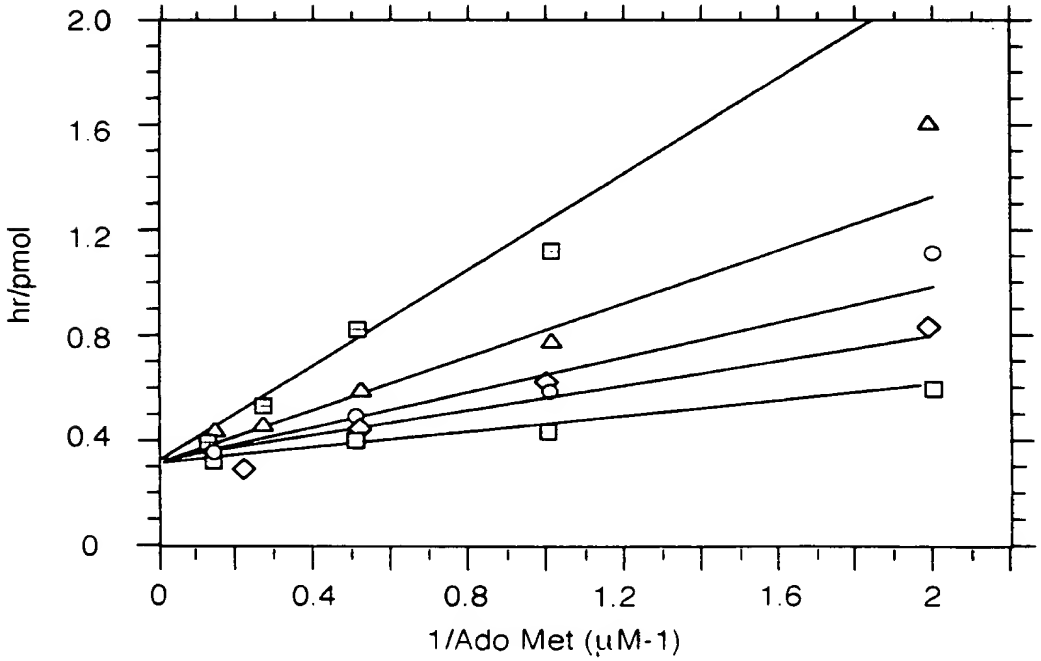

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FIG. 15.

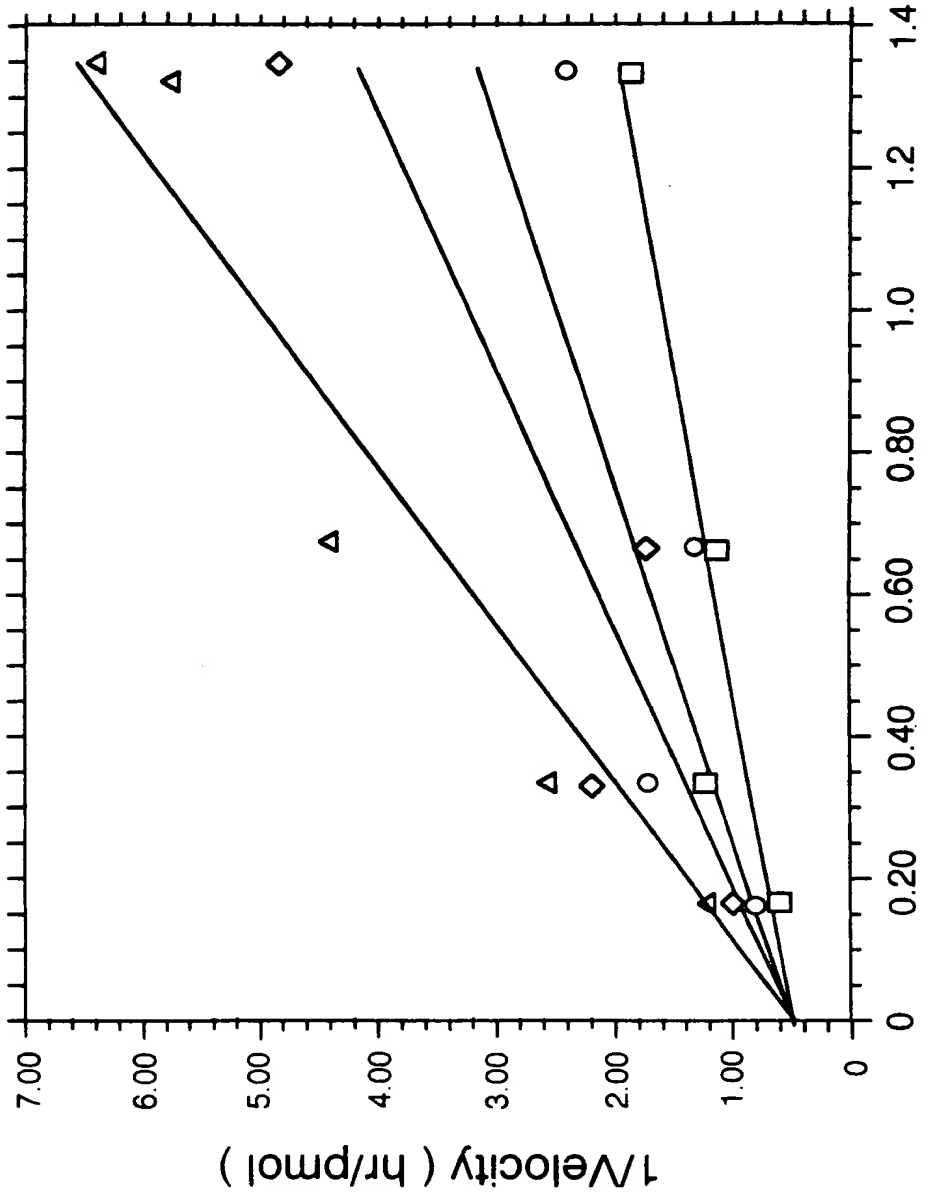

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FIG. 17a.

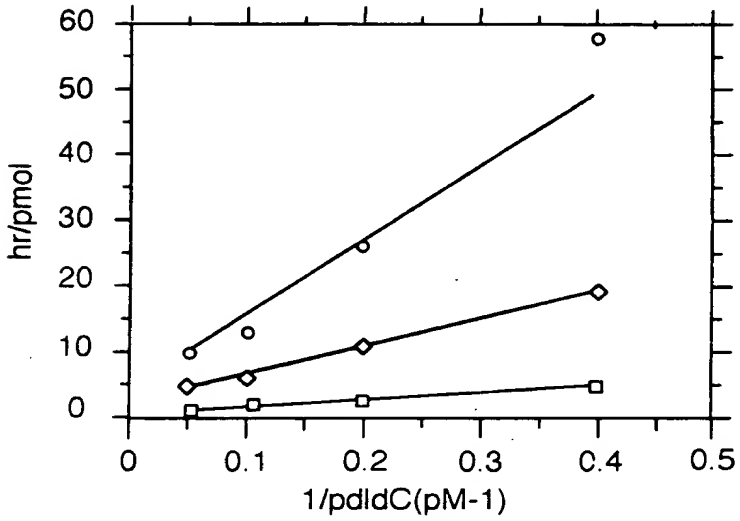

FIG. 17b.

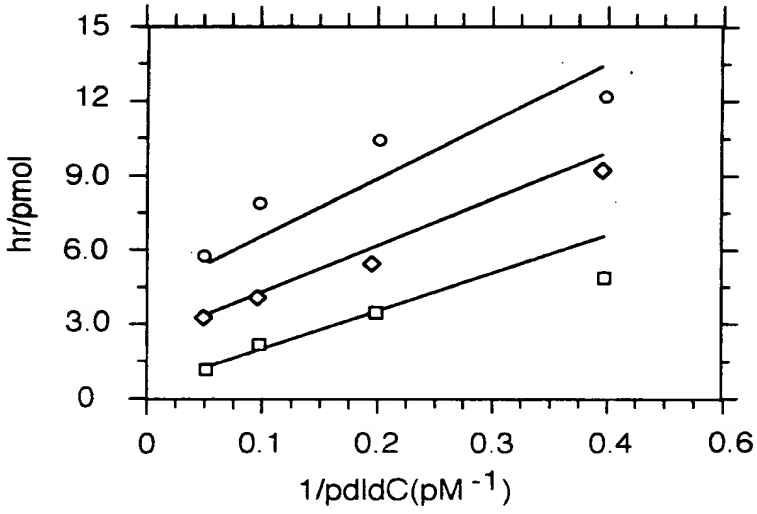

FIG. 17c.

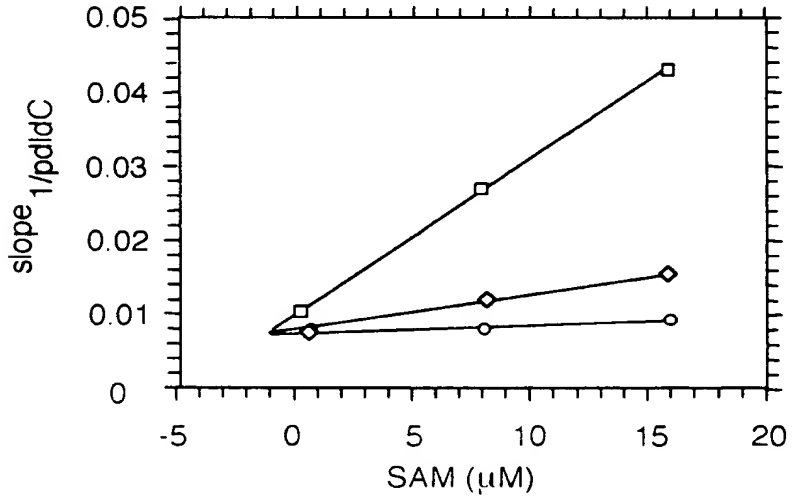

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FIG. 18.

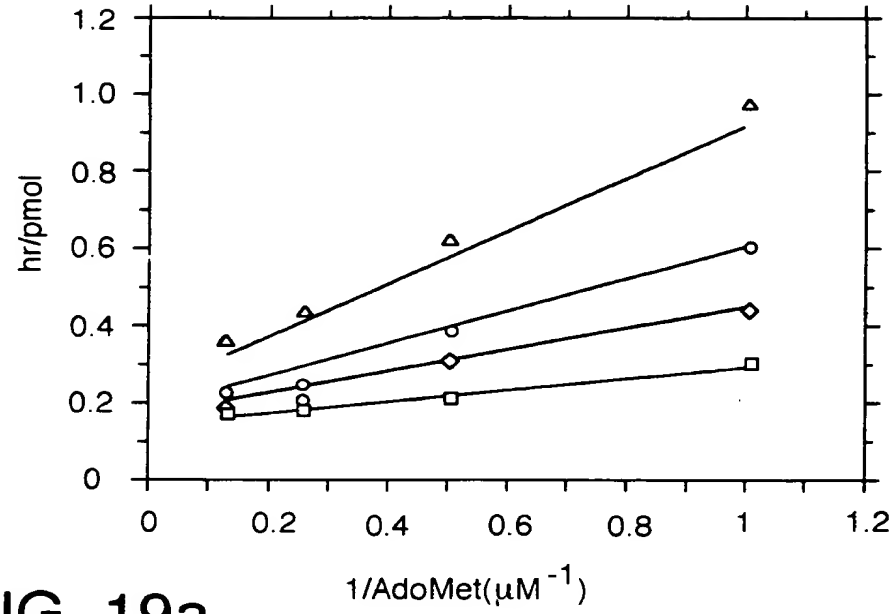

FIG. 19a.

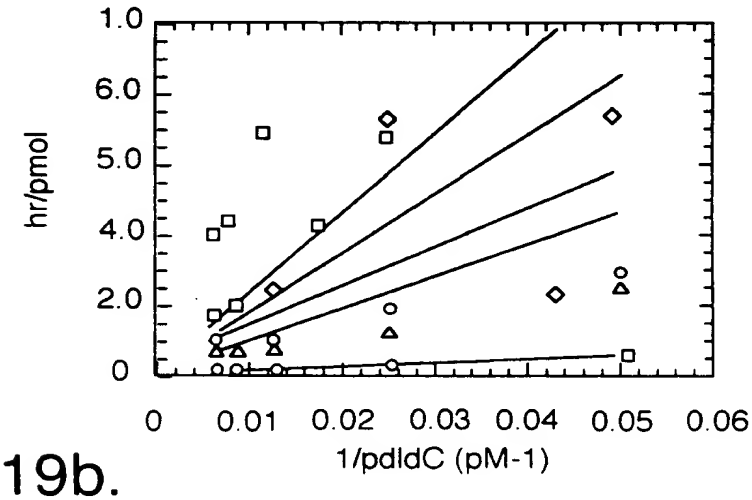

FIG. 19b.

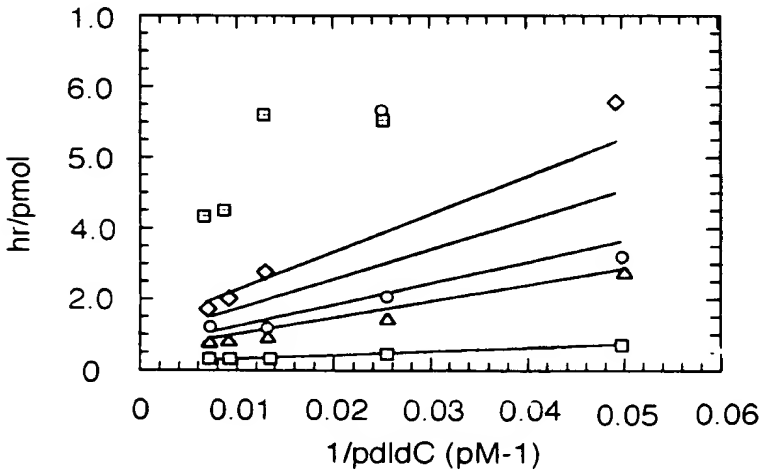

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FIG.20.

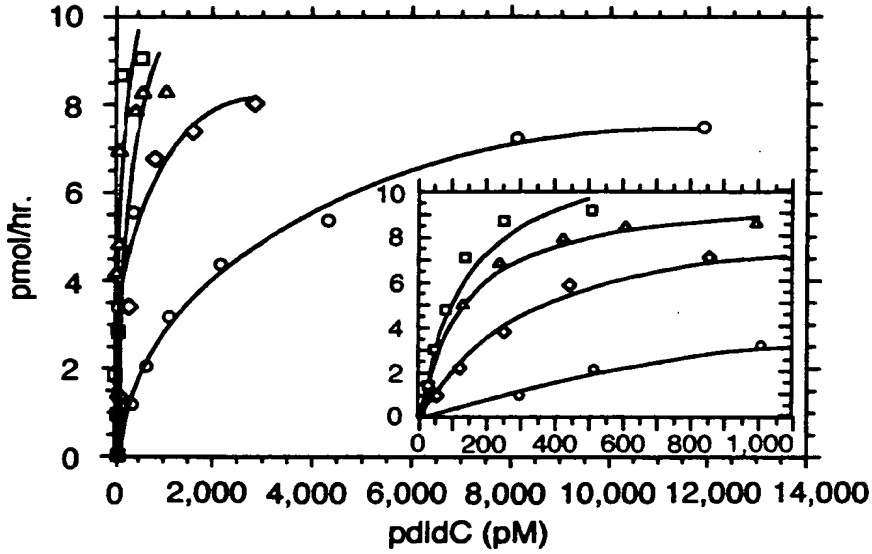

FIG.21.

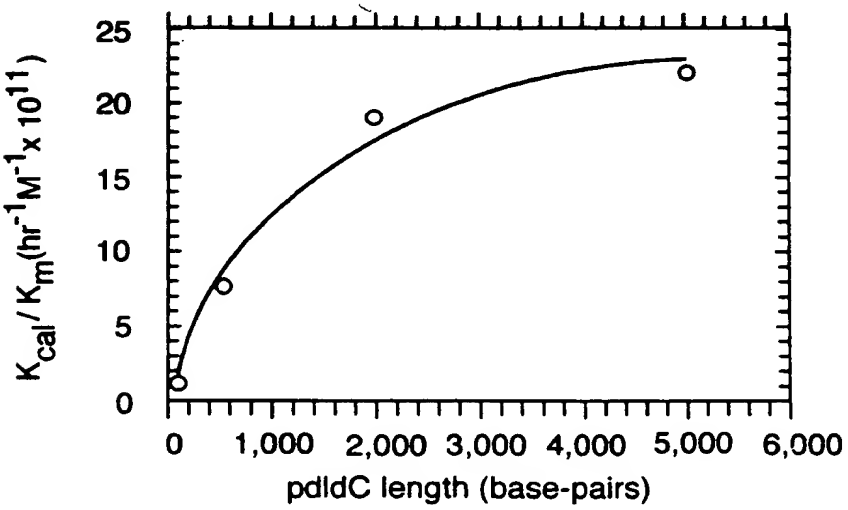

FIG.22.

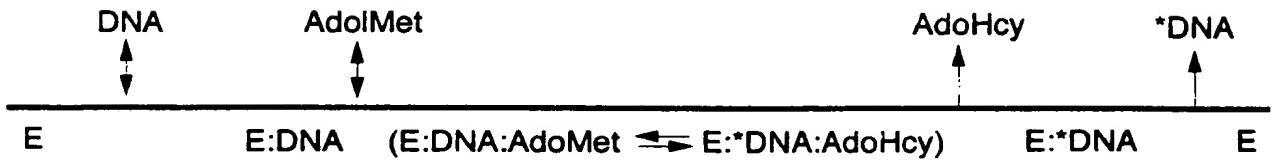

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FIG.23a.

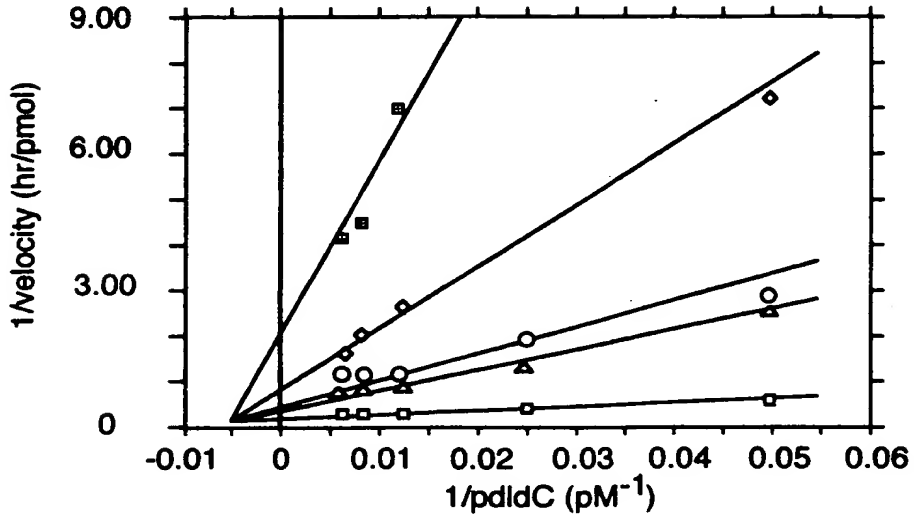

FIG.23b.

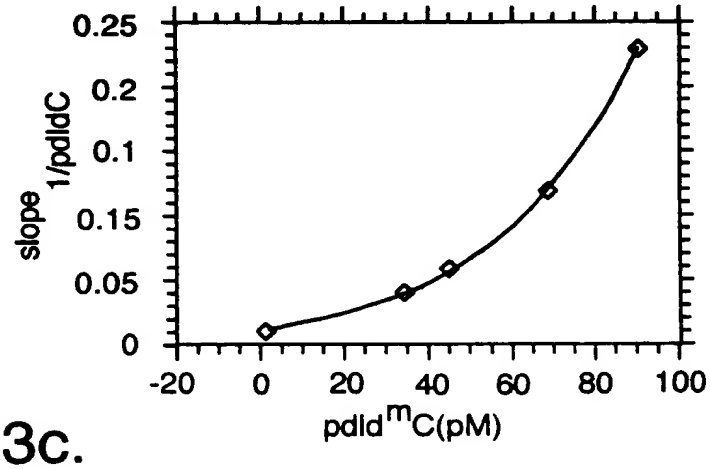

FIG.23c.